

**FIGURE 1****A.****SEQ ID NO:1 - Hu1 light chain variable region amino acid sequence**

EIVLTQSPDFQSVTPKEKVTITCRASQFVGSSIHQYQQKPDQSPKLLIKYASESMS  
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

**B.****SEQ ID NO:2 - Hu1 light chain variable region nucleic acid sequence**

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA  
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTCAAGCATCCACTG  
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT  
GAGTCTATGTCTGGGGTCCCCTCGAGGTTCAGTGGCAGTGGATCTGGGACAG  
ATTTACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC  
TGTCACAAAGTCATAGCTGGCATTTCACGTTCGGCCAAGGGACCAAGGTGG  
AAATCAAA

**FIGURE 2****A.****SEQ ID NO:3 - Hu1 heavy chain variable region amino acid sequence**

EVQLVESGGGLVQPGGSLRLSCAASGFTFSNHWMNWVRQAPGKGLEWVGEIRS  
KSINSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSTY  
DHWGQGTTLVTVSS

**B.****SEQ ID NO:4 - Hu1 heavy chain variable region nucleic acid sequence**

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGATTCACTTTCAGTAACCACTGGATGAAC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT  
CAAAATCTATTAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT  
CACCATCTCAAGAGATGATTCAAAGAAGTCACTGTACCTGCAGATGAACAGC  
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA  
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

**FIGURE 3****A.****SEQ ID NO:5 - A10K light chain variable region amino acid sequence**

EIVLTQSPDFQSVTPKEKVTITCRASQFVGYSIHWYQQKPDQSPKLLIKYASESRS  
GVPSRFSGSGSGTDFTLTINSLEAEDAATYYCQQSHSWHFTFGQGTKVEIK

**B.****SEQ ID NO:6 - A10K light chain variable region nucleic acid sequence**

GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGA  
AAGTCACCATCACCTGCAGGGCCAGTCAGTTCGTTGGCTATAGCATCCACTG  
GTACCAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGTATGCTTCT  
GAGTCTAGGTCTGGGGTCCCCTCGAGGTTCA GTGGCAGTGGATCTGGGACAG  
ATTTACCCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTAC  
TGTCACAAAGTCATAGCTGGCATTTCACGTTCCGCCAAGGGACCAAGGTGG  
AAATCAAA

**FIGURE 4****A.****SEQ ID NO:7 - A10K heavy chain amino acid sequence**

EVQLVESGGGLVQPGGSLRLSCAASGFKFSNHWMNWVRQAPGKGLEWVGEIRS  
KSMNSATHYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGST  
YDHWGQGTLVTVSS

**B.****SEQ ID NO:8 - A10K heavy chain nucleic acid sequence**

GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCC  
TGAGACTCTCCTGTGCAGCCTCTGGATTCCCTTTCAGTAACCACTGGATGAAC  
TGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTTGGCGAAATTAGAT  
CAAAATCTATGAATTCTGCAACACATTATGCGGAGTCTGTGAAAGGGAGATT  
CACCATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGC  
CTGAAAACCGAGGACACGGCCGTGTATTACTGTGCTAGAAATTACTACGGTA  
GTACCTACGACCATTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

**FIGURE 5****A. Amino acid sequence of a human light chain framework region with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:57) (CDRL1) (FRL2 - SEQ ID NO:58) (CDRL2)  
 EIVLTQSPDFQSVTPKEKVTITCXXXXXXXXXXXXWYQKPDQSPKLLIKXXXXXXXX  
 (FRL3 - SEQ ID NO:59) (CDRL3) (FRL4 - SEQ ID NO:60)  
 GVPSRFGSGSGTDFLTINSLEAEDAATYYCXXXXXXXXXXFGQGTVKVEIK

**B. Nucleic acid sequence of a human light chain framework region with interspersed CDR sequences labeled**

(FRL1 - SEQ ID NO:61)  
 GAAATTGTGCTGACTCAGTCTCCAGACTTTCAGTCTGTGACTCCAAAAGAGAAAG  
 (CDRL1)  
 TCACCATCACCTGCXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTGGTAC  
 (FRL2 - SEQ ID NO:62) (CDRL2)  
 CAGCAGAAGCCAGATCAGTCTCCAAAGCTCCTCATCAAGXXXXXXXXXXXXXXXX  
 (CDRL2 cont.) (FRL3 - SEQ ID NO:63)  
 XXXXXXXGGGGTCCCCTCGAGGTTTCAGTGGCAGTGGATCTGGGACAGATTTCAC  
 CCTCACCATCAATAGCCTGGAAGCTGAAGATGCTGCCACGTATTACTGT  
 (CDRL3) (FRL4 - SEQ ID NO:64)  
 XXXXXXXXXXXXXXXXXXXXXXXXXXXXXTTCGGCCAAGGGACCAAGGTGGAAA  
 TCAAA

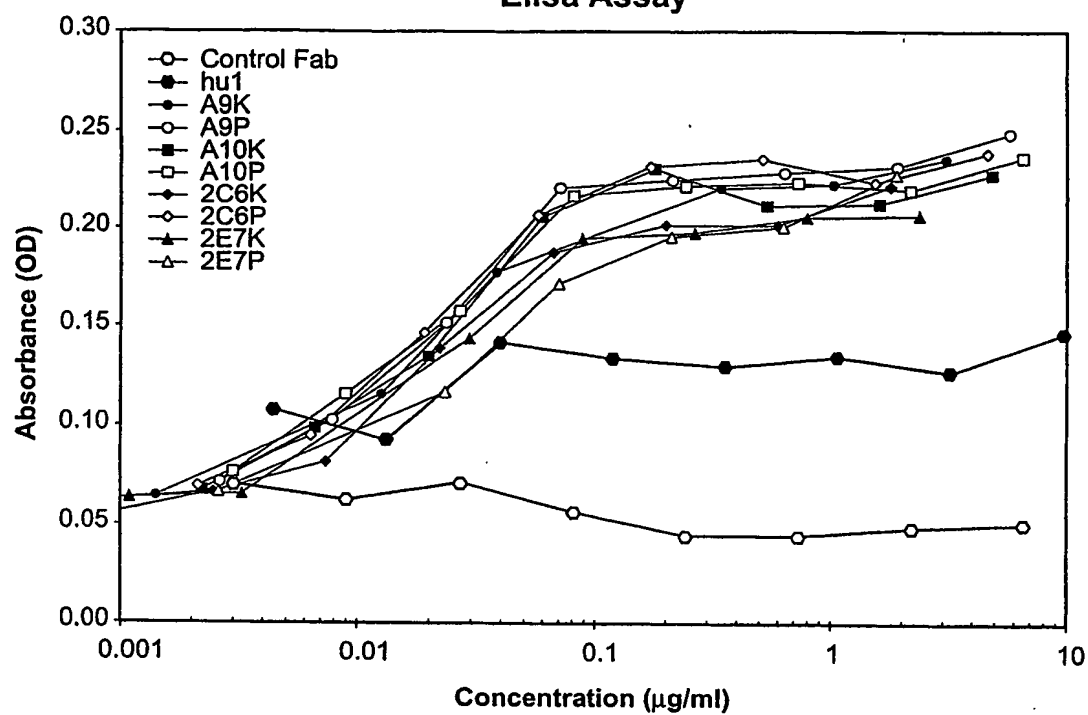
**FIGURE 6****A. Amino acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:65) (CDRH1) (FRH2 - SEQ ID NO:66)  
 EVQLVESGGGLVQPGGSLRLSCAASXXXXXXXXXXXXWVRQAPGKGLEWVG  
 (CDRH2) (FRH3 - SEQ ID NO:67)  
XXXXXXXXXXXXXXXXXXXXRFTISRDDSKNSLYLQMNSLKTEDTAVYYCAR  
 (CDRH3) (FRH4 - SEQ ID NO:68)  
XXXXXXXXXXWGQGTLLTVSS

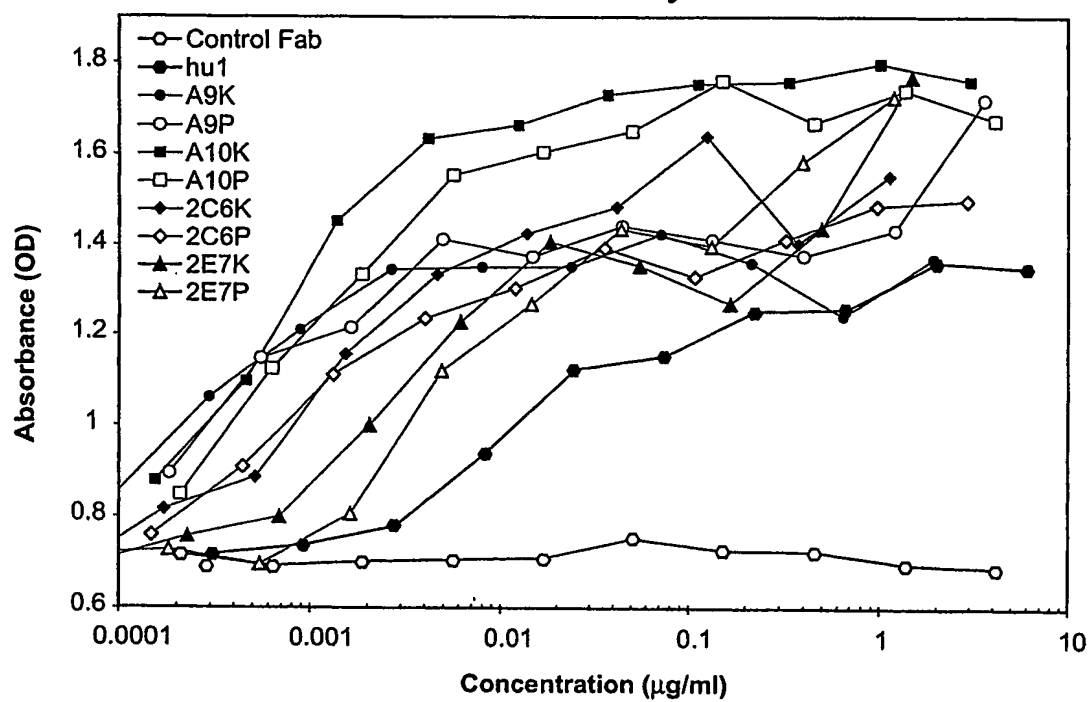
**B. Nucleic acid sequence of a human heavy chain framework region with interspersed CDR sequences labeled**

(FRH1 - SEQ ID NO:69)  
 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTCCAGCCTGGAGGGTCCCTG  
 (CDRH1)  
 AGACTCTCCTGTGCAGCCTCTXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXTG  
 (FRH2 - SEQ ID NO:70) (CDRH2)  
 GGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTGGCXXXXXXXXXXXXXXXX  
 (CDRH2 cont.)  
XXAGATTCAC  
 (FRH3 - SEQ ID NO:71)  
 CATCTCAAGAGATGATTCAAAGAACTCACTGTACCTGCAGATGAACAGCCTGAA  
 (CDRH3)  
 AACCGAGGACACGGCCGTGTATTACTGTGCTAGXXXXXXXXXXXXXXXXXXXX  
 (CDRH3) (FRH4 - SEQ ID NO:72)  
XXXXXXXXXXTGGGGCCAAGGGACCCTGGTCACCGTCTCCTCA

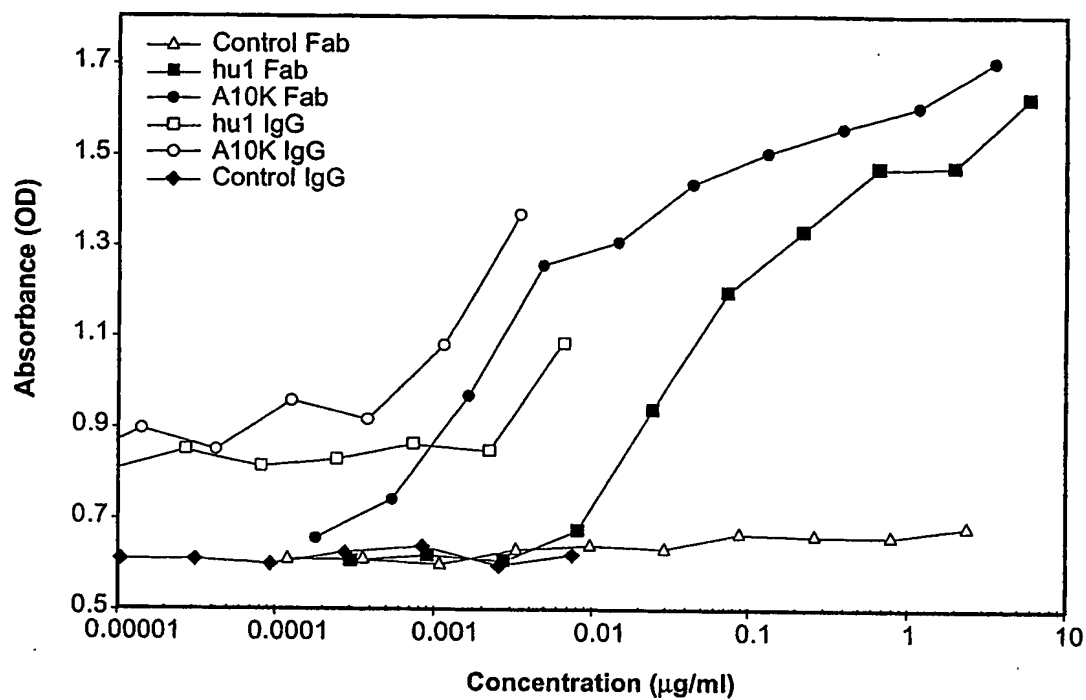
**FIGURE 7**  
**Elisa Assay**



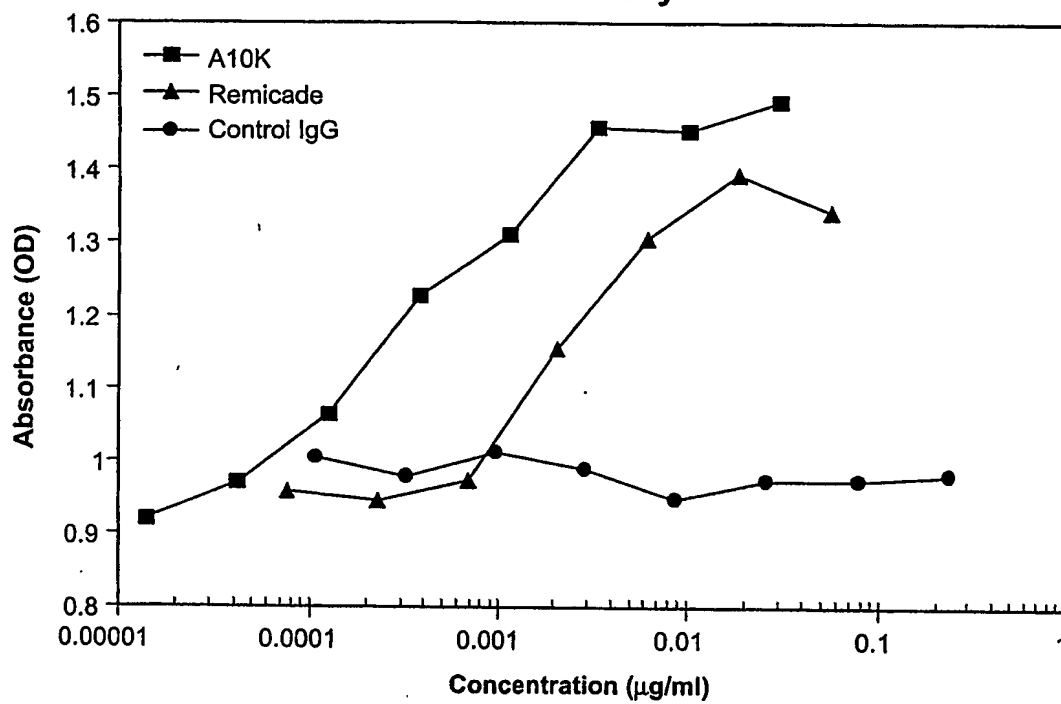
**FIGURE 8**  
**L929 Assay**



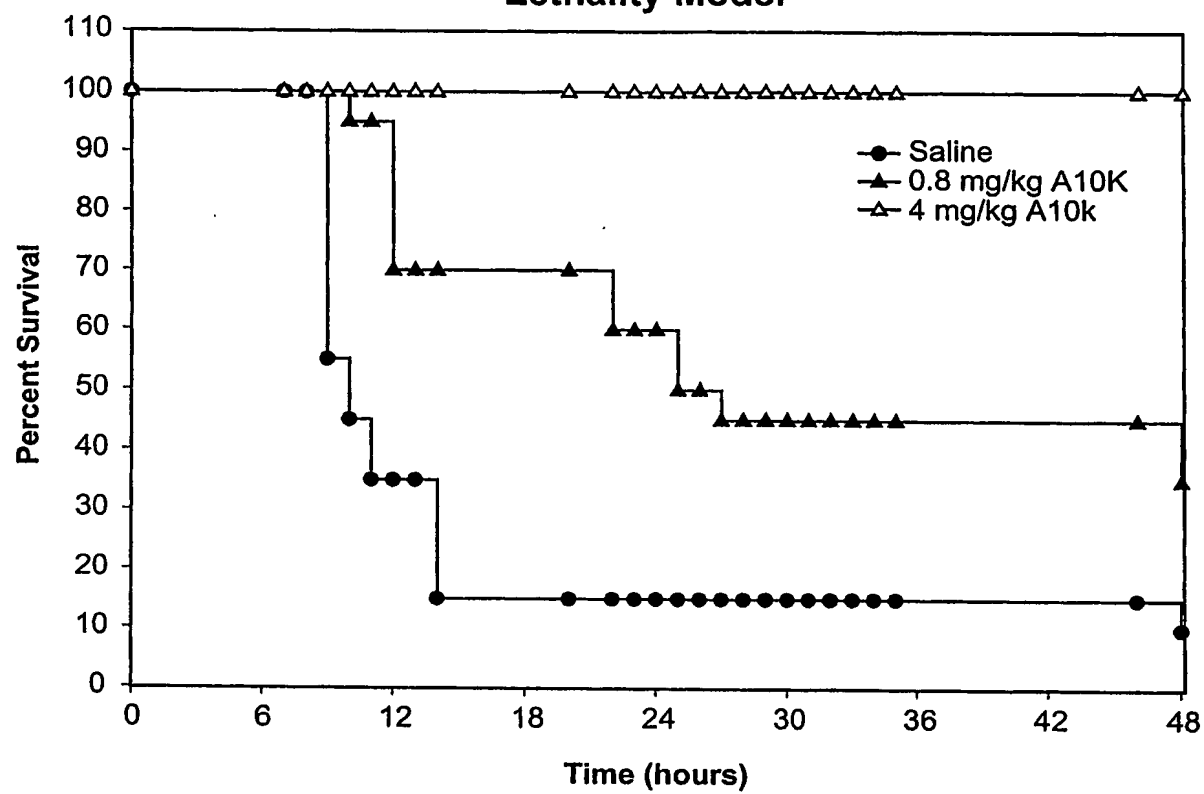
**FIGURE 9**  
**L929 Assay**



**FIGURE 10**  
**L929 Assay**



**FIGURE 11**  
**Lethality Model**



**FIGURE 12**  
**Polyarthritis Model**

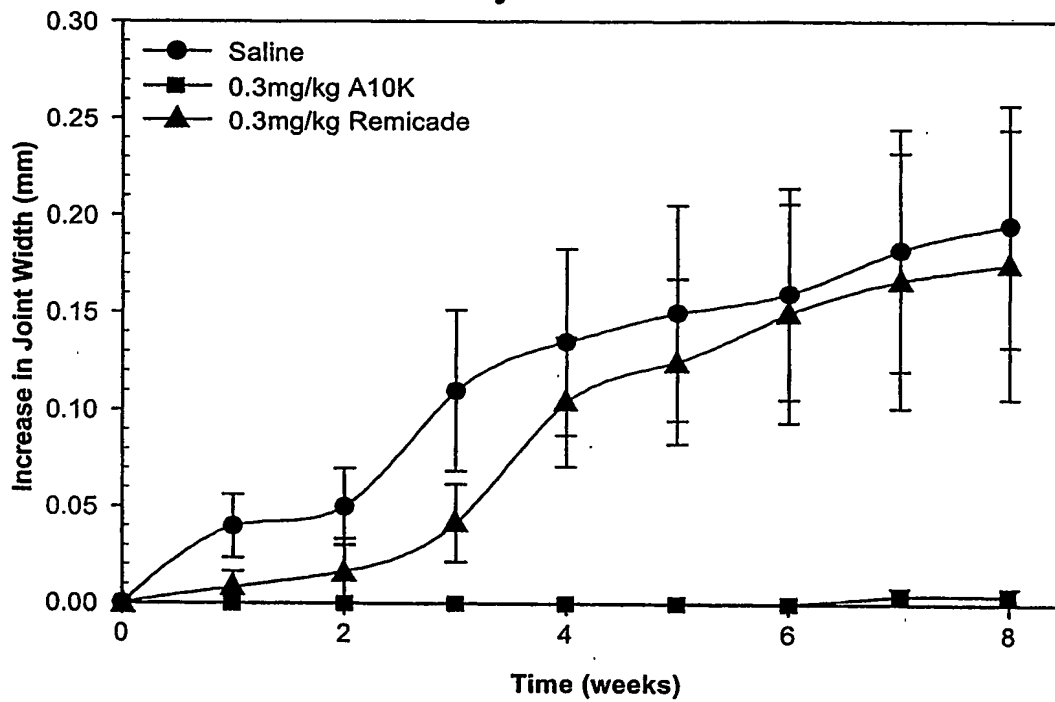
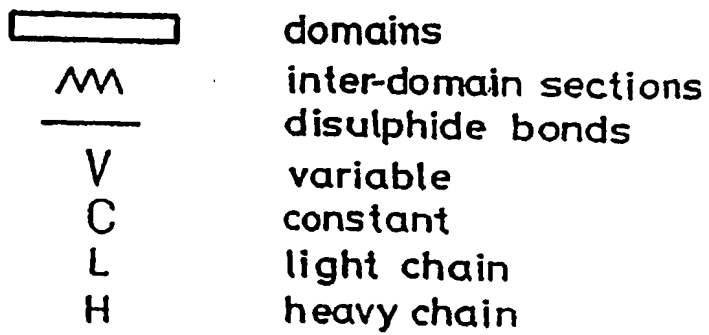
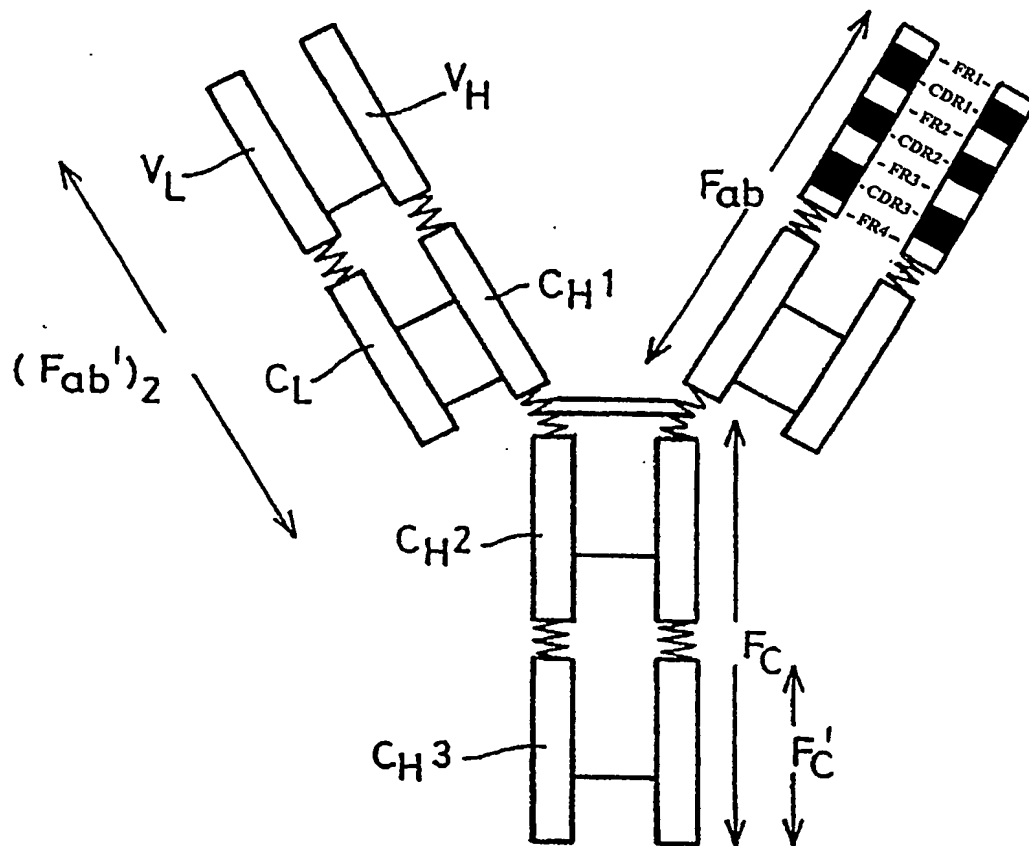


FIGURE 13



**FIGURE 14****A. SEQ ID NO:85 - Human CL Sequence**

TCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAG  
CACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCC  
GAACCGGTGACGGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGCACA  
CCTTCCCGGCTGTCCTACAGTCTCTCAGGACTCTACTCCCTCAGCAGCGTGGTG  
ACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAATC  
ACAAGCCCAGCAACACCAAGGTGGACAAGAAAGCAGAGGCCCAAATCTTCT  
ACTAGTGTTCCTACCCATATGATGTACCTGATTATGCATCATAG

Note: This CH1 sequence contains the first six IgG1 hinge region residues (in bold) and fused to a HA decapeptide tag (*italic*) through a four amino acid linker (underlined).

**B. SEQ ID NO:86 - Human CH1 Sequence**

CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTT  
GAAATCTGGAAGTGCCTCTGTTGTGTGCTGCTGAATAACTTCTATCCCAGAG  
AGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCA  
GGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAG  
CACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC  
GAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCAACAGGG  
GAGAGTCTTAG

**FIGURE 15****A.****SEQ ID NO:109 - AME 3-2 Complete Heavy Chain**

EVQLVESGGGLVQPGGSLRLSCAASGFTFRNHWMNWVRQAPGKGLEWVGEIR  
SKSINSATFYAESVKGRFTISRDDSKNSLYLQMNSLKTEDTAVYYCARNYYGSY  
YDHWGQGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVS  
WNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVD  
KRVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSH  
EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK  
CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPS  
DIAVEWESNGQPENNYKTTTPVLDSGDSFFLYSKLTVDKSRWQQGNVFSCSVMH  
EALHNHYTQKSLSLSPGK\*

**B.****SEQ ID NO:110 - AME 3-2 Complete Light Chain**

DIQMTQSPSSLSASVGDRVTITCVTTQFVGYAIHWYQQKPGKAPKLLIYYASSR  
SGVPSRFSGSGSGTDFLTITSLQPEDFATYYCQQSHGWPFTFGQGTKVEIKRTV  
AAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVT  
EQDSKDSTYLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC\*